

MOLECULAR DIVERGENCE AND HOST RELATIONSHIPS IN NEW ZEALAND REPRESENTATIVES OF THE PEA CRAB GENUS *PINNOTHERES*

The Pinnotheridae is a family of decapod crustaceans comprising more than 120 mostly microphagous and commensal species. As symbionts of a variety of aquatic invertebrates, pinnotherids typically live in an intimate association with their host depending on it for an almost lifelong source of nourishment and shelter, together with a site for mating. The New Zealand pinnotherid fauna was thought to comprise only one species, *Pinnotheres novaezelandiae* Filhol, associated with a multitude of hosts. Recently, however, a separate species, *P. atrinicola* Page, has been described which is regarded as being host specific to the horse mussel *Atrina zelandica* Gray (Page, 1983, 1984). The biological status of the groups of crabs ascribed to the taxon *P. novaezelandiae*, but found within different host species in New Zealand waters is the focus of this paper.

Results

The biological status of the taxon *P. novaezelandiae* was investigated by a survey of electrophoretically detectable genetic variation of populations from throughout the North Island of New Zealand. Pea crabs from 11 host populations from six geographically disparate localities were subjected to cellulose acetate and poly-acrylamide electrophoresis. Forty-one enzyme systems were screened for polymorphism. Clearly resolved enzyme phenotypes were obtained at 23 presumptive loci, of which 15 exhibited polymorphism.

An analysis of electromorph frequency data revealed *P. novaezelandiae* is highly genetically structured and typified by high levels of polymorphism, results atypical of brachyuran crabs (mean proportion of loci polymorphic 99% criterion, $P = 41.51$; mean expected heterozygosity $H_E = 0.142$). Of particular significance, is the pattern of genetic differentiation observed among populations of *P. novaezelandiae*. Hierarchical F-statistics (Wright, 1978) indicated that the preponderance of inter-population differentiation can be attributed to differences in electromorph frequency among host-associated populations of *P. novaezelandiae* within a sampling locality ($F_{PI} = 0.261$, $F_{LR} = -0.0115$, $F_{RT} = -0.003$; where P = Population, L = Locality, R = Region) (Stevens, 1990a). In addition, heterogeneity χ^2 analyses indicated significant deviations from homogeneity among host-associated populations within a locality. For example, populations from the Manukau Harbour and the Bay of Islands exhibited significant heterogeneity at 80% and 46.6% of non-monomorphic loci respectively. Geographic differentiation was thus a comparatively insignificant factor in the structuring of the sampled *P. novaezelandiae* populations. Individuals belonging to two genetically very distinct units were found within a newly recorded host species, *Maetra ovata ovata* Gray at Green and Wood Bays, Manukau Harbour (minimum genetic distance separation from other *P. novaezelandiae* $D = 0.214$ and 0.046 respectively) (Stevens, in press B). A Hardy-Weinberg and F-statistic analysis of populations nom-

inally *P. novaezelandiae* found in three different species of hosts (*Perna canaliculus*, *Mytilus edulis aoteanus*, *Chione stuechburyi*) at Opuha, Bay of Islands 1986–1990 indicated the host-associated populations of *P. novaezelandiae* exhibited such a pronounced pattern of homozygote excess, differentiation and disturbance from genetic equilibrium in sympatry that it is unreasonable to consider them as a single panmictic population (Stevens, in press A).

Discussion

It is concluded that significant genetical (and hence biological) discontinuities based on host origin exist within the currently recognised taxon. Such a conclusion is supported by qualitative differences in host recognition observed between different host-associated populations of *P. novaezelandiae* (Stevens, 1990b). Conservatively these discontinuities indicate host race development, although a viable alternate hypothesis would be the presence of cryptic, host-specific biological species within *P. novaezelandiae*.

Acknowledgements

I thank Dr D.M. Lambert for invaluable advice and assistance. This research was supported by grants 449.215 and 449.219 from the Auckland University Research Committee (to D.M. Lambert and P.M. Stevens) and from the New Zealand Mussel Farming Association (to P.M. Stevens)

Literature Cited

- Page, R.D.M. 1983. Description of a new species of *Pinnotheres*, and a redescription of *Pinnotheres novaezelandiae* (Brachyura: Pinnotheridae). *New Zealand Journal of Zoology* 10: 151–162.
1984. 'Systematics of the pea crabs (Genus *Pinnotheres*) of New Zealand (Brachyura: Pinnotheridae)'. Unpublished M.Sc. Thesis, University of Auckland, Auckland, New Zealand. 87p.
- Stevens, P.M. 1990a. A genetic analysis of the pea crabs (Decapoda: Pinnotheridae) of New Zealand I: patterns of spatial and host-associated genetic structuring in *Pinnotheres novaezelandiae* Filhol. *Journal of Experimental Marine Biology and Ecology* 141(2/3): 195–212.
- 1990b. Specificity of host recognition of individuals from different host races of symbiotic pea crabs (Decapoda: Pinnotheridae). *Journal of Experimental Marine Biology and Ecology* 143(3): 193–208.
- In Press A. Molecular divergence in pea crabs (Decapoda: Pinnotheridae): a case of host-associated genetic discontinuities in marine symbionts. *Heredity*.
- In Press B. New host record for pea crabs (*Pinnotheres* spp.) symbiotic with bivalve molluscs in New Zealand.
- Wright, S. 1978. 'Evolution and the genetics of populations'. (University of Chicago Press: Chicago).

P.M. Stevens, Department of Zoology, Evolutionary Genetics Laboratory, University of Auckland, Private Bag, Auckland, New Zealand.